(1) GENERAL INFORMATION:

(i) APPLICANTS: Goodearl, Andrew; Stroobant, Paul; Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark; Chen, Maio Su; Hiles, Ian

(ii) TITLE OF INVENTION: Glial Mitogenic Factors, Their Preparation and Use

(iii) NUMBER OF SEQUENCES: 184

(iv) CORRESPONDENCE ADDRESS:
    (A) ADDRESSEE: Felfe & Lynch
    (B) STREET: 805 Third Avenue
    (C) CITY: New York City
    (D) STATE: New York
    (E) COUNTRY: USA
    (F) ZIP: 10022

(v) COMPUTER READABLE FORM:
    (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
    (B) COMPUTER: IBM
    (C) OPERATING SYSTEM: PC-DOS
    (D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:
    (A) APPLICATION NUMBER:
    (B) FILING DATE:
    (C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: 08/036,555
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(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: 07/965,173
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(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: 07/940,389
    (B) FILING DATE: 03-SEP-1992

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    (B) FILING DATE: 30-JUN-1992

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(vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER:  U.K. 91 07566.3
      (B) FILING DATE:  10-APRIL-1991

(viii) ATTORNEY/AGENT INFORMATION:
      (A) NAME:  Tsai, Christine H.
      (B) REGISTRATION NUMBER:  34,266
      (C) REFERENCE/DOCKET NUMBER:  LUD 5250.17

(ix) TELECOMMUNICATION INFORMATION:
      (A) TELEPHONE: (212) 688-9200
      (B) TELEFAX: (212) 838-3884


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    1:
    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH:    8
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY:  linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:


Phe Lys Gly Asp Ala His Thr Glu
 1                   5



(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    2:
    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH:    13
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY:  linear
    (ix)  FEATURE:
      (D)  OTHER INFORMATION:  Xaa in position 1 is Lysine or Arginine;
                              Xaa in position 12 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:


Xaa Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys
 1               5                   10
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 3:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 12
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ix) FEATURE:
          (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
                                    Xaa in position 10 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Xaa Thr Glu Thr Ser Ser Ser Gly Leu Xaa Leu Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 4:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 9
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ix) FEATURE:
          (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Xaa Lys Leu Gly Glu Met Trp Ala Glu
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 5:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 7
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ix) FEATURE:
          (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Xaa Leu Gly Glu Lys Arg Ala
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 6:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 16
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
      (ix) FEATURE:
           (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Xaa Ile Lys Ser Glu His Ala Gly Leu Ser Ile Gly Asp Thr Ala Lys
 1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 7:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 13
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
      (ix) FEATURE:
           (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Xaa Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 8:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 16
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear
      (ix) FEATURE:
           (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Xaa Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys
 1   5   10   15

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 9:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 13
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
     (ix) FEATURE:
          (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine
                                    and Xaa in position 12 is unknown.
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Xaa Met Ser Glu Tyr Ala Phe Phe Val Gln Thr Xaa Arg
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 10:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 14
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
     (ix) FEATURE:
          (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Xaa Ser Glu His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 11:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 10
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
     (ix) FEATURE:
          (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
                                    Xaa in position 8 is unknown.
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Xaa Ala Gly Tyr Phe Ala Glu Xaa Ala Arg
 1   5   10

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 12:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
                                   Xaa in position 7 is unknown.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Xaa Lys Leu Glu Phe Leu Xaa Ala Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 13:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 11
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Xaa Thr Thr Glu Met Ala Ser Glu Gln Gly Ala
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 14:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginin .
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Xaa Ala Lys Glu Ala Leu Ala Ala Leu Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 15:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 8
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear
        (ix) FEATURE:
                (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Xaa Phe Val Leu Gln Ala Lys Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 16:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 6
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear
        (ix) FEATURE:
                (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Xaa Leu Gly Glu Met Trp
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 17:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 16
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Glu Tyr Lys Cys Leu Lys Phe Lys Trp Phe Lys Lys Ala Thr Val Met
 1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 18:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: Xaa in position 8 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Glu Ala Lys Tyr Phe Ser Lys Xaa Asp Ala
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 19:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 7
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: Xaa in position 2 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Glu Xaa Lys Phe Tyr Val Pro
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 20:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Glu Leu Ser Phe Ala Ser Val Arg Leu Pro Gly Cys Pro Pro Gly Val
 1   5   10   15

Asp Pro Met Val Ser Phe Pro Val Ala Leu
      20   25

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 21:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 2003

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear ·

    (ix) FEATURE:

        (D)   OTHER INFORMATION: N in positions 31 and 32 could be either A or G.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:


```
GGAATTCCTT TTTTTTTTTT TTTTTTTCTT NNTTTTTTTT TGCCCTTATA CCTCTTCGCC          60
TTTCTGTGGT TCCATCCACT TCTTCCCCCT CCTCCTCCCA TAAACAACTC TCCTACCCCT         120
GCACCCCCAA TAAATAAATA AAAGGAGGAG GGCAAGGGGG GAGGAGGAGG AGTGGTGCTG         180
CGAGGGGAAG GAAAAGGGAG GCAGCGCGAG AAGAGCCGGG CAGAGTCCGA ACCGACAGCC         240
AGAAGCCCGC ACGCACCTCG CACC ATG AGA TGG CGA CGC GCC CCG CGC CGC          291
                           Met Arg Trp Arg Arg Ala Pro Arg Arg
                            1               5

TCC GGG CGT CCC GGC CCC CGG GCC CAG CGC CCC GGC TCC GCC GCC CGC          339
Ser Gly Arg Pro Gly Pro Arg Ala Gln Arg Pro Gly Ser Ala Ala Arg
 10              15                  20                  25

TCG TCG CCG CCG CTG CCG CTG CTG CCA CTA CTG CTG CTG CTG GGG ACC          387
Ser Ser Pro Pro Leu Pro Leu Leu Pro Leu Leu Leu Leu Leu Gly Thr
            30                  35                  40

GCG GCC CTG GCG CCG GGG GCG GCG GCC GGC AAC GAG GCG GCT CCC GCG          435
Ala Ala Leu Ala Pro Gly Ala Ala Ala Gly Asn Glu Ala Ala Pro Ala
            45                  50                  55

GGG GCC TCG GTG TGC TAC TCG TCC CCG CCC AGC GTG GGA TCG GTG CAG          483
Gly Ala Ser Val Cys Tyr Ser Ser Pro Pro Ser Val Gly Ser Val Gln
            60                  65                  70

GAG CTA GCT CAG CGC GCC GCG GTG GTG ATC GAG GGA AAG GTG CAC CCG          531
Glu Leu Ala Gln Arg Ala Ala Val Val Ile Glu Gly Lys Val His Pro
        75                  80                  85

CAG CGG CGG CAG CAG GGG GCA CTC GAC AGG AAG GCG GCG GCG GCG GCG          579
Gln Arg Arg Gln Gln Gly Ala Leu Asp Arg Lys Ala Ala Ala Ala Ala
 90                  95                  100                 105

GGC GAG GCA GGG GCG TGG GGC GGC GAT CGC GAG CCG CCA GCC GCG GGC          627
Gly Glu Ala Gly Ala Trp Gly Gly Asp Arg Glu Pro Pro Ala Ala Gly
                110                 115                 120

CCA CGG GCG CTG GGG CCG CCC GCC GAG GAG CCG CTG CTC GCC GCC AAC          675
Pro Arg Ala Leu Gly Pro Pro Ala Glu Glu Pro Leu Leu Ala Ala Asn
            125                 130                 135
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GGG ACC GTG CCC TCT TGG CCC ACC GCC CCG GTG CCC AGC GCC GGC GAG          723
Gly Thr Val Pro Ser Trp Pro Thr Ala Pro Val Pro Ser Ala Gly Glu
        140             145                 150

CCC GGG GAG GAG GCG CCC TAT CTG GTG AAG GTG CAC CAG GTG TGG GCG          771
Pro Gly Glu Glu Ala Pro Tyr Leu Val Lys Val His Gln Val Trp Ala
        155             160                 165

GTG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG CTC ACC GTG CGC CTG          819
Val Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu Leu Thr Val Arg Leu
170             175                 180             185

GGG ACC TGG GGC CAC CCC GCC TTC CCC TCC TGC GGG AGG CTC AAG GAG          867
Gly Thr Trp Gly His Pro Ala Phe Pro Ser Cys Gly Arg Leu Lys Glu
                190                 195                 200

GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAC GCC AAC AGC ACC AGC          915
Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Asp Ala Asn Ser Thr Ser
                205                 210                 215

CGC GCG CCG GCC GCC TTC CGA GCC TCT TTC CCC CCT CTG GAG ACG GGC          963
Arg Ala Pro Ala Ala Phe Arg Ala Ser Phe Pro Pro Leu Glu Thr Gly
        220             225                 230

CGG AAC CTC AAG AAG GAG GTC AGC CGG GTG CTG TGC AAG CGG TGC GCC          1011
Arg Asn Leu Lys Lys Glu Val Ser Arg Val Leu Cys Lys Arg Cys Ala
        235             240                 245

TTG CCT CCC CAA TTG AAA GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT          1059
Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly
250             255                 260             265

TCC AAA CTA GTC CTT CGG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC          1107
Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
                270                 175                 180

AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA AAA AAC AAA          1155
Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys
                185                 190                 195

CCA CAA AAT ATC AAG ATA CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC          1203
Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg
        200             205                 210

ATT AAC AAA GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG TGC AAA GTG          1251
Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val
        215             220                 225

ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG          1299
Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val
230             235                 240             245
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GAA TCA AAC GCT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA        1347
Glu Ser Asn Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val
                250                         255                 260

AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC        1395
Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
                265                         270                 275

TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG TGC AAG TGC        1443
Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
                280                         285                 290

CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC        1491
Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser
                295                     300                 305

TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA                    1530
Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
400                         405                 410

TAGGAGCATG CTCAGTTGGT GCTGCTTTCT TGTTGCTGCA TCTCCCCTCA GATTCCACCT      1590
AGAGCTAGAT GTGTCTTACC AGATCTAATA TTGACTGCCT CTGCCTGTCG CATGAGAACA      1650
TTAACAAAAG CAATTGTATT ACTTCCTCTG TTCGCGACTA GTTGGCTCTG AGATACTAAT      1710
AGGTGTGTGA GGCTCCGGAT GTTTCTGGAA TTGATATTGA ATGATGTGAT ACAAATTGAT      1770
AGTCAATATC AAGCAGTGAA ATATGATAAT AAAGGCATTT CAAAGTCTCA CTTTTATTGA      1830
TAAAATAAAA ATCATTCTAC TGAACAGTCC ATCTTCTTTA TACAATGACC ACATCCTGAA      1890
AAGGGTGTTG CTAAGCTGTA ACCGATATGC ACTTGAAATG ATGGTAAGTT AATTTTGATT      1950
CAGAATGTGT TATTTGTCAC AAATAAACAT AATAAAAGGA AAAAAAAAAA AAA            2003
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 22:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 11 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys
 1   5   10

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 23:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 11
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (ix) FEATURE:
            (D)   OTHER INFORMATION: Xaa in position 9 is unknown.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Thr Glu Thr Ser Ser Ser Gly Leu Xaa Leu Lys
  1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 24:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 12
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
  1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 25:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 9
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (ix) FEATURE:
            (D)   OTHER INFORMATION: Xaa in position 7 is unknown.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Ala Gly Tyr Phe Ala Glu Xaa Ala Arg
  1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 26:
       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 10
              (B) TYPE: amino acid
              (C) STRANDEDNESS:
              (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Thr Thr Glu Met Ala Ser Glu Gln Gly Ala
  1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 27:
       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 9
              (B) TYPE: amino acid
              (C) STRANDEDNESS:
              (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Ala Lys Glu Ala Leu Ala Ala Leu Lys
  1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 28:
       (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 7
              (B) TYPE: amino acid
              (C) STRANDEDNESS:
              (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Phe Val Leu Gln Ala Lys Lys
  1   5

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 29:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: lin ar
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Glu Thr Gln Pro Asp Pro Gly Gln Ile Leu Lys Lys Val Pro Met Val
 1   5   10   15

Ile Gly Ala Tyr Thr
                20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 30:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: Xaa in positions 1, 3, 17 and 19 is
                                    unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Xaa Glu Xaa Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys Glu
 1   5   10   15

Xaa Gly Xaa Gly Lys
                20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 31:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 32:
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 8
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (ix) FEATURE:
            (D)   OTHER INFORMATION: Xaa in position 6 is unknown.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Lys Leu Glu Phe Leu Xaa Ala Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 33:
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 9
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (ix) FEATURE:
            (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Xaa Val His Gln Val Trp Ala Ala Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 34:
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 14
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (ix) FEATURE:
            (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine,
                                      Xaa in position 11 is unknown.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Xaa Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 35:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 14
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (ix) FEATURE:
            (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine,
                                      Xaa in position 13 is unknown.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Xaa Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 36:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 9
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (ix) FEATURE:
            (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Xaa Trp Phe Val Val Ile Glu Gly Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 37:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 16
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (ix) FEATURE:
            (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Xaa Ala Ser Pro Val Ser Val Gly Ser Val Gln Glu Leu Val Gln Arg
 1   5   10   15

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 38:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 13
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (ix) FEATURE:
            (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Xaa Val Cys Leu Leu Thr Val Ala Ala Leu Pro Pro Thr
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 39:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 7
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (ix) FEATURE:
            (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
                                      Xaa in position 6 is unknown.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Xaa Asp Leu Leu Leu Xaa Val
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 40:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 39
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Cys Thr Cys Gly Cys Cys Lys Cys Cys Arg Thr Thr Cys Ala Cys Arg
 1   5   10   15

Cys Ala Gly Ala Ala Gly Gly Thr Cys Thr Thr Cys Thr Cys Cys Thr
                 20   25   30

Thr Cys Thr Cys Ala Gly Cys
             35

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 41:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 24
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Cys Cys Thr Cys Gly Cys Thr Cys Cys Thr Thr Cys Thr Thr Cys Thr
 1   5   10   15

Thr Gly Cys Cys Cys Thr Thr Cys
               20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 42:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 60
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

AAGTGCCCAA ATGAGTTTAC TGGTGATCGC TGCCAAAACT ACGTAATGGC CAGCTTCTAC   60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 43:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 36
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AGTACGTCCA CTCCCTTTCT GTCTCTGCCT GAATAG   36

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 44:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 569
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

AAGGCGGAGG AGCTGTACCA GAAGAGAGTG CTGACCATAA CCGGCATCTG CATCGCCCTC   60
CTTGTGGTCG GCATCATGTG TGTGGTGGCC TACTGCAAAA CCAAGAAACA GCGGAAAAAG   120
CTGCATGACC GTCTTCGGCA GAGCCTTCGG TCTGAACGAA ACAATATGAT GAACATTGCC   180
AATGGGCCTC ACCATCCTAA CCCACCCCCC GAGAATGTCC AGCTGGTGAA TCAATACGTA   240
TCTAAAAACG TCATCTCCAG TGAGCATATT GTTGAGAGAG AAGCAGAGAC ATCCTTTTCC   300
ACCAGTCACT ATACTTCCAC AGCCCATCAC TCCACTACTG TCACCCAGAC TCCTAGCCAC   360
AGCTGGAGCA ACGGACACAC TGAAAGCATC CTTTCCGAAA GCCACTCTGT AATCGTGATG   420
TCATCCGTAG AAAACAGTAG GCACAGCAGC CCAACTGGGG GCCCAAGAGG ACGTCTTAAT   480
GGCACAGGAG GCCCTCGTGA ATGTAACAGC TTCCTCAGGC ATGCCAGAGA AACCCCTGAT   540
TCCTACCGAG ACTCTCCTCA TAGTGAAAG   569

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 45:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 8
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Val His Gln Val Trp Ala Ala Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 46:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 13
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
        (ix) FEATURE:
            (D)   OTHER INFORMATION: Xaa in position 10 is unknown.
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
 1   5   10

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 47:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 13
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
    (ix) FEATURE:
          (D)   OTHER INFORMATION: Xaa in position 12 is unknown.
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

L u Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 48:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 8
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Trp Phe Val Val Ile Glu Gly Lys
1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 49:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 15
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Ala Ser Pro Val Ser Val Gly Ser Val Gln Glu Leu Val Gln Arg
1   5   10   15

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 50:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 12
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Val Cys Leu Leu Thr Val Ala Ala Leu Pro Pro Thr
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 51:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 9
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Lys Val His Gln Val Trp Ala Ala Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 52:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 13
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear
        (ix) FEATURE:
                (D)   OTHER INFORMATION: Xaa in position 12 is unknown.
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lys
 1   5   10

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 53:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 6
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 5 is unknown.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Asp Leu Leu Leu Xaa Val
  1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 54:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TTYAARGGNG AYGCNCAYAC   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 55:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CATRTAYTCR TAYTCRTCNG C   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 56:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TGYTCNGANG CCATYTCNGT   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 57:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TGYTCRCTNG CCATYTCNGT   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 58:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CCDATNACCA TNGGNACYTT   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 59:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GCNGCCCANA CYTGRTGNAC   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 60:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GCYTCNGGYT CCATRAARAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 61:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CCYTCDATNA CNACRAACCA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 62:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 17
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

TCNGCRAART ANCCNGC   17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 63:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GCNGCNAGNG CYTCYTTNGC   20

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 64:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20
        (B) TYPE: nucl ic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GCNGCYAANG CYTCYTTNGC   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 65:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTYTTNGCYT GNAGNACRAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 66:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

TTYTTNGCYT GYAANACRAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 67:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TGNACNAGYT CYTGNAC   17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 68:
  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 17
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

TGNACYAAYT CYTGNAC   17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 69:
  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 21
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CATRTAYTCN CCNGARTCNG C   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 70:
  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 21
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CATRTAYTCN CCRCTRTCNG C   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 71:
  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 21
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

NGARTCNGCY AANGANGCYT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 72:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 21
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

NGARTCNGCN AGNGANGCYT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 73:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 21
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

RCTRTCNGCY AANGANGCYT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 74:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 21
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

RCTRTCNGCN AGNGANGCYT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 75:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 21
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

NGARTCNGCY AARCTNGCYT T   21

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 76:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 21
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

NGARTCNGCN AGRCTNGCYT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 77:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 730
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GTATGTGTCA GCCATGACCA CCCCGGCTCG TATGTCACCT GTAGATTTCC ACACGCCAAG   60
CTCCCCCAAA TCGCCCCCTT CGGAAATGTC TCCACCCGTG TCCAGCATGA CGGTGTCCAT   120
GCCTTCCATG GCGGTCAGCC CCTTCATGGA AGAAGAGAGA CCTCTACTTC TCGTGACACC   180
ACCAAGGCTG CGGGAGAAGA AGTTTGACCA TCACCCTCAG CAGTTCAGCT CCTTCCACCA   240
CAACCCCGCG CATGACAGTA ACAGCCTCCC TGCTAGCCCC TTGAGGATAG TGGAGGATGA   300
GGAGTATGAA ACGACCCAAG AGTACGAGCC AGCCCAAGAG CCTGTTAAGA AACTCGCCAA   360
TAGCCGGCGG GCCAAAAGAA CCAAGCCCAA TGGCCACATT GCTAACAGAT TGGAAGTGGA   420
CAGCAACACA AGCTCCCAGA GCAGTAACTC AGAGAGTGAA ACAGAAGATG AAAGAGTAGG   480
TGAAGATACG CCTTTCCTGG GCATACAGAA CCCCCTGGCA GCCAGTCTTG AGGCAACACC   540
TGCCTTCCGC CTGGCTGACA GCAGGACTAA CCCAGCAGGC CGCTTCTCGA CACAGGAAGA   600
AATCCAGGCC AGGCTGTCTA GTGTAATTGC TAACCAAGAC CCTATTGCTG TATAAAACCT   660
AAATAAACAC ATAGATTCAC CTGTAAAACT TTATTTTATA TAATAAAGTA TTCCACCTTA   720
AATTAAACAA   730

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 78:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 21
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

RCTRTCNGCY AARCTNGCYT T   21

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 79:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: nucl ic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

RCTRCTNGCN AGRCTNGCYT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 80:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ACNACNGARA TGGCTCNNGA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 81:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ACNACNGARA TGGCAGYNGA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 82:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CAYCARGTNT GGGCNGCNAA   20

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 83:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 20
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TTYGTNGTNA THGARGGNAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 84:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 20
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

AARGGNGAYG CNCAYACNGA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 85:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 20
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GARGCNYTNG CNGCNYTNAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 86:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 20
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

GTNGGNTCNG TNCARGARYT   20

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 87:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

GTNGGNAGYG TNCARGARYT   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 88:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

NACYTTYTTN ARDATYTGNC C   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 89:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 417
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: Xaa in positions 14, 23, 90, 100, 126,
                   and 135 is a stop codon.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TCTAA AAC TAC AGA GAC TGT ATT TTC ATG ATC ATC ATA GTT CTG TGA AAT ATA   53
     Asn Tyr Arg Asp Cys Ile Phe Met Ile Ile Ile Val Leu Xaa Asn Ile
     1   5   10   15

CTT AAA CCG CTT TGG TCC TGA TCT TGT AGG AAG TCA GAA CTT CGC ATT   101
Leu Lys Pro Leu Trp Ser Xaa Ser Cys Arg Lys Ser Glu Leu Arg Ile
     20   25   30

AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC   149
Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Ser Met Cys Lys Val Ile
     35   40   45

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AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG        197
Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Arg Ile Val Glu
    50              55                  60

TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA        245
Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Il  Ser Gln Ser Leu Arg
65              70                  75                  80

GGA GTG ATC AAG GTA TGT GGT CAC ACT TGA ATC ACG CAG GTG TGT GAA        293
Gly Val Ile Lys Val Cys Gly His Thr Xaa Ile Thr Gln Val Cys Glu
                85                  90                  95

ATC TCA TTG TGA ACA AAT AAA AAT CAT GAA AGG AAA ACT CTA TGT TTG        341
Il  Ser Cys Xaa Thr Asn Lys Asn His Glu Arg Lys Thr Leu Cys Leu
        100                 105                 110

AAA TAT CTT ATG GGT CCT CCT GTA AAG CTC TTC ACT CCA TAA GGT GAA        389
Lys Tyr Leu Met Gly Pro Pro Val Lys Leu Phe Thr Pro Xaa Gly Glu
        115                 120                 125

ATA GAC CTG AAA TAT ATA TAG ATT ATT T                                  417
Ile Asp Leu Lys Tyr Ile Xaa Ile Ile
    130                 135
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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 90:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: N at positions 19, 25, and 31 is Inosine.
                                 Y can be cytidine or thymidine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

CCGAATTCTG CAGGARACNC ARCCNGAYCC NGG   33

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 91:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: N at positions 14, 20, 23, 29, and 35 is
                          Inosine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

AAGGATCCTG CAGNGTRTAN GCNCCDATNA CCATNGG   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 92:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 34
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: N at positions 16, 21, and 24 is Inosine.
                          Y can be cytidine or thymidine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CCGAATTCTG CAGGCNGAYT CNGGNGARTA YATG   34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 93:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: N at positions 16 and 25 is Inosine. Y
                          can be cytidine or thymidine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CCGAATTCTG CAGGCNGAYA GYGGNGARTA YAT   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 94:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 34
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ix) FEATURE:
            (D)   OTHER INFORMATION: N at positions 14, 15, 16, 26, and 29 is
                                      Inosine. Y can be cytidine or thymidine.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

AAGGATCCTG CAGNNNCATR TAYTCNCCNG ARTC   34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 95:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 34
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ix) FEATURE:
            (D)   OTHER INFORMATION: N at positions 14, 15, 16, and 26 is
                                      Inosine. Y can be cytidine or thymidine.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAGGATCCTG CAGNNNCATR TAYTCNCCRC TRTC   34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 96:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 33
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ix) FEATURE:
            (D)   OTHER INFORMATION: N at positions 21, 28, and 31 is Inosine.
                                      Y can be cytidine or thymidine.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CCGAATTCTG CAGCAYCARG TNTGGGCNGC NAA   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 97:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 35
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
      (ix) FEATURE:
           (D)   OTHER INFORMATION: N at position 31 is Inosine. Y can be
                                     cytidine or thymidine.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CCGAATTCTG CAGATHTTYT TYATGGARCC NGARG   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 98:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 35
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
      (ix) FEATURE:
           (D)   OTHER INFORMATION: N at positions 18, 21, 24, 27, and 33 is
                                     Inosine. Y can be cytidine or thymidine.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CCGAATTCTG CAGGGGGNCC NCCNGCNTTY CCNGT   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 99:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 33
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
      (ix) FEATURE:
           (D)   OTHER INFORMATION: N at positions 21 and 24 is Inosin . Y
                                     can be cytidine or thymidine.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CCGAATTCTG CAGTGGTTYG TNGTNATHGA RGG   33

135

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 100:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 35
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (ix) FEATURE:
                (D)   OTHER INFORMATION: N at positions 17, 20, and 26 is Inosine.
                                         Y can be cytidine or thymidine.
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

AAGGATCCTG CAGYTTNGCU NGCCCANACY TGRTG   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 101:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 33
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (ix) FEATURE:
                (D)   OTHER INFORMATION: N at position 19 is Inosine. Y can be
                                         cytidine or thymidine.
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

AAGGATCCTG CAGGCYTCNG GYTCCATRAA RAA   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 102:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 33
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (ix) FEATURE:
                (D)   OTHER INFORMATION: N at positions 16, 22, 25, 28, and 31 is
                                         Inosine.
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

AAGGATCCTG CAGACNGGRA ANGCNGGNGG NCC   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 103:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 35
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D) OTHER INFORMATION: N at positions 17, 26, and 29 is Inosine.
                                  Y can be cytidine or thymidine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

AAGGATCCTG CAGYTTNCCY TCDATNACNA CRAAC   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 104:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D) OTHER INFORMATION: N at position 18 is Inosine. Y can be
                                  cytidine or thymidine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CATRTAYTCR TAYTCTCNGC AAGGATCCTG CAG   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 105:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D) OTHER INFORMATION: N at position 19, 25, and 31 is Inosine.
                                Y can be cytidine or thymidine.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CCGAATTCTG CAGAARGGNG AYGCNCAYAC NGA   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 106:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: N at position 3 and 18 is Inosine. Y can
                                                be cytidine or thymidine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

GCNGCYAANG CYTCYTTNGC AAGGATCCTG CAG   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 107:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: N at position 3, 6, 9, and 18 is Inosine.
                                          Y can be cytidine or thymidine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GCNGCNAGNG CYTCYTTNGC AAGGATCCTG CAG   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 108:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: N at position 3, 12, and 15 is Inosine.Y
                                          can be cytidine or thymidine.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

TCNGCRAART ANCCNGCAAG GATCCTGCAG   30

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 109:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 38
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CATCGATCTG CAGGCTGATT CTGGAGAATA TATGTGCA   38

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 110:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

AAGGATCCTG CAGCCACATC TCGAGTCGAC ATCGATT   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 111:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CCGAATTCTG CAGTGATCAG CAAACTAGGA AATGACA   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 112:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 37
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

CATCGATCTG CAGCCTAGTT TGCTGATCAC TTTGCAC   37

139

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 113:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 37
                (B) TYPE: nucl ic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

AAGGATCCTG CAGTATATTC TCCAGAATCA GCCAGTG   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 114:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 34
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

AAGGATCCTG CAGGCACGCA GTAGGCATCT CTTA   34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 115:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 35
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

CCGAATTCTG CAGCAGAACT TCGCATTAGC AAAGC   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 116:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 33
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

CATCCCGGGA TGAAGAGTCA GGAGTCTGTG GCA   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 117:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 39
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: singl
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATACCCGGGC TGCAGACAAT GAGATTTCAC ACACCTGCG   39

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 118:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 36
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AAGGATCCTG CAGTTTGGAA CCTGCCACAG ACTCCT   36

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 119:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 39
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

ATACCCGGGC TGCAGATGAG ATTTCACACA CCTGCGTGA   39

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 120:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 12
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

His Gln Val Trp Ala Ala Lys Ala Ala Gly Leu Lys
 1   5   10

141

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 121:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 16
             (B) TYPE: amino acid
             (C) STRANDEDNESS:
             (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Gly Gly Leu Lys Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Ala Asn
 1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 122:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 13
             (B) TYPE: amino acid
             (C) STRANDEDNESS:
             (D) TOPOLOGY: linear
      (ix) FEATURE:
             (D)   OTHER INFORMATION: Xaa in position 12 is unknown.
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 123:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 23
             (B) TYPE: amino acid
             (C) STRANDEDNESS:
             (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

 Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser
  1   5   10   15

 Cys Gly Arg Leu Lys Glu Asp
            20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 124:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 13
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear
        (ix) FEATURE:
                (D)   OTHER INFORMATION: Xaa in position 10 is unknown.
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 125:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 23
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu Ala Asn Ser
 1   5   10   15
Ser Gly Gly Pro Gly Arg Leu
                20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 126:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 14
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser
 1   5   10

143

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 127:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```
Glu Tyr Lys Cys Leu Lys Phe Lys Trp Phe Lys Lys Ala Thr Val Met
1               5                   10                  15
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 128:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

```
Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys
1               5                   10                  15
Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys
            20                  25
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 129:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in position 12 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

```
Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lys
1               5                   10
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 130:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 23
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met
 1   5   10   15

Cys Lys Val Ile Ser Lys Leu
                20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 131:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 12
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 132:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 22
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

L u Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
 1   5   10   15

Lys Val Ile Ser Lys Leu
                20

145

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 133:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 744
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: singl
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:


```
CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG   55
        His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
        1                   5                   10                  15

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC           103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
        20                  25                  30

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG          151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
        35                  40                  45

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC           199
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro
    50                  55                  60

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG           247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val
65                  70                  75                  80

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG           295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
            85                  90                  95

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA           343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
            100                 105                 110

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC           391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser
            115                 120                 125

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG           439
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys
        130                 135                 140

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT           487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr
145                 150                 155                 160

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC           535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
                165                 170                 175
```

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```
ATC ACC ATT GTG GAG TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT          583
Ile Thr Ile Val Glu Ser Asn Gly Lys Arg Cys L u L u Arg Ala Il
            180                     185                 190


TCT CAG TCT CTA AGA GGA GTG ATC AAG GTA TGT GGT CAC ACT              625
Ser Gln Ser Leu Arg Gly Val Ile Lys Val Cys Gly His Thr
        195                     200                 205


TGAATCACGC AGGTGTGTGA AATCTCATTG TGAACAAATA AAAATCATGA AAGGAAAAAA      685
AAAAAAAAAA AATCGATGTC GACTCGAGAT GTGGCTGCAG GTCGACTCTA GAGGATCCC       744
```

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CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG   55
        His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
        1             5               10                  15

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC           103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
        20              25                  30

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG          151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
        35              40                  45

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC          199
Ala Lys Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro
    50                  55                  60

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG          247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val
65                  70                  75                  80

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG          295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
                85                  90                  95

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA          343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
            100                 105                 110
```

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```
TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC        391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser
        115             120             125

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG        439
Arg Lys Asn Lys Gly Gly Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys
    130             135             140

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT        487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr
145             150             155             160

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC        535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
            165             170             175

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA        583
Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr
            180             185             190

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT        631
Ser His Leu Val Lys Ser Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
            195             200             205

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC        679
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
        210             215             220

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT        727
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
225             230             235             240

GTG CCC ATG AAA GTC CAA ACC CAA GAA AGT GCC CAA ATG AGT TTA CTG        775
Val Pro Met Lys Val Gln Thr Gln Glu Ser Ala Gln Met Ser Leu Leu
            245             250             255

GTG ATC GCT GCC AAA ACT ACG TAATGGCCAG CTTCTACAGT ACGTCCACTC          826
Val Ile Ala Ala Lys Thr Thr
            260


CCTTTCTGTC TCTGCCTGAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC     886
TCCCCTCAGA TTCCTCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCTCT     946
GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC CGTGACTAGT     1006
GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG ATCTTGAATT     1066
ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA     1126
GTCAAAAAAA AAAAAAAAAA AAAAAATCGA TGTCGACTCG AGATGTGGCT GCAGGTCGAC     1186
TCTAGAG                                                               1193
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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 135:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1108
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:


```
CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG   55
        His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
        1           5               10                  15

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC           103
L u Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
            20              25              30

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG           151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
            35              40              45

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC           199
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro
    50              55              60

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG           247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val
65              70              75              80

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG           295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
            85              90              95

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA           343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
            100             105             110

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC           391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser
            115             120             125

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG           439
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Pro Lys
    130             135             140

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT           487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr
145             150             155             160

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC           535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
            165             170             175
```

149

```
ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA        583
Ile Arg Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr
            180             185             190

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT        631
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
            195             200             205

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC        679
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
    210             215             220

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC        727
L u Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
225             230             235             240

GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT        775
Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro
            245             250             255

GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC TCCCCTCAGA TTCCGCCTAG  838
Glu

AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCTCT GCCTGTCGCA TGAGAACATT        898
AACACAAGCG ATTGTATGAC TTCCTCTGTC CGTGACTAGT GGGCTCTGAG CTACTCGTAG        958
GTGCGTAAGG CTCCAGTGTT TCTGAAATTG ATCTTGAATT ACTGTGATAC GACATGATAG       1018
TCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA GTCAAAAAAA AAAAAAAAAA       1078
AAAAATCGAT GTCGACTCGA GATGTGGCTG                                       1108
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 136:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 559
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D)   OTHER INFORMATION: N in position 214 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```
AGTTTCCCCC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC         60
GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC        120
TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC        180
CCAGCGGCGC GCCAGCAGGA GCCACCCCGC GAGNCGTGCG ACCGGGACGG AGCGCCCGCC        240
AGTCCCAGGT GGCCCGGACC GCACGTTGCG TCCCCGCGCT CCCCGCCGGC GACAGGAGAC        300
GCTCCCCCCC ACGCCGCGCG CGCCTCGGCC CGGTCGCTGG CCCGCCTCCA CTCCGGGGAC        360
AAACTTTTCC CGAAGCCGAT CCCAGCCCTC GGACCCAAAC TTGTCGCGCG TCGCCTTCGC        420
CGGGAGCCGT CCGCGCAGAG CGTGCACTTC TCGGGCGAG ATG TCG GAG CGC AGA         474
                                           Met Ser Glu Arg Arg
                                           1                 5
```

150

```
GAA GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG          522
Glu Gly Lys Gly Lys Gly Lys Gly Gly Lys Lys Asp Arg Gly Ser Gly
                 10                      15                  20

AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG.AGC CCA G                        559
Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala
             25                  30
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 137:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 252
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: N in position 8 could be either A or G.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```
CC CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG           47
   His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser
    1           5               10                  15

CTG CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC          95
Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser
                 20                  25                  30

TGC GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC          143
Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro
                 35                  40                  45

GAG GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC          191
Glu Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro
                 50                  55                  60

CCC TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT          239
Pro Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala
         65                  70                  75

GTG CAA CGG TGC G                                                        252
Val Gln Arg Cys
    80
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 138:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 178
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

CCT TGC CTC CCC GCT TGA AAG AGA TGA AGA GTC AGG AGT CTG TGG CAG   48
Leu Pro Pro Arg Leu Lys Glu His Lys Ser Gln Glu Ser Val Ala Gly
1   5   10   15

GTT CCA AAC TAG TGC TTC GGT GCG AGA CCA GTT CTG AAT ACT CCT CTC   96
Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
            20   25   30

TCA AGT TCA AGT GGT TCA AGA ATG GGA GTG AAT TAA GCC GAA AGA ACA   144
Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys
            35   40   45

AAC CAC AAA ACA TCA AGA TAC AGA AAA GGC CGG G   178
Pro Gly Asn Ile Lys Ile Gln Lys Arg Pro Gly
        50   55

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 139:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 122
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA   46
  Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly
  1   5   10   15

GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT   94
Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser
            20   25   30

GCC AAC ATC ACC ATT GTG GAG TCA AAC G   122
Ala Asn Ile Thr Ile Val Glu Ser Asn Ala
        35

152

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 140:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 417
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```
TCTAAAACTA CAGAGACTGT ATTTTCATGA TCATCATAGT TCTGTGAAAT ATACTTAAAC          60
CGCTTTGGTC CTGATCTTGT AGG AAG TCA GAA CTT CGC ATT AGC AAA GCG             110
                         Lys Ser Glu Leu Arg Ile Ser Lys Ala
                          1               5

TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA          158
Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu
 10               15                  20                  25

GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GGT          206
Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Gly
                 30                  35                  40

AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA GGA GTG ATC          254
Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg Gly Val Ile
             45                  50                  55

AAG GTA TGT GGT CAC ACT TGAATCACGC AGGTGTGTGA AATCTCATTG                  302
Lys Val Cys Gly His Thr
             60

TGAACAAATA AAAATCATGA AAGGAAAACT CTATGTTTGA AATATCTTAT GGGTCCTCCT        362
GTAAAGCTCT TCACTCCATA AGGTGAAATA GACCTGAAAT ATATATAGAT TATTT             417
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 141:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 102
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

```
AG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT           47
Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser
 1               5                  10                  15

TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT          95
Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr
                 20                  25                  30

TCT TCA T                                                                102
Ser Ser Ser
         35
```

153

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 142:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 69
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT GTG CCC   48
Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro
 1   5   10   15

ATG AAA GTC CAA ACC CAA GAA   69
Met Lys Val Gln Thr Gln Glu
            20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 143:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 60
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG   48
Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met
 1   5   10   15

GCC AGC TTC TAC   60
Ala Ser Phe Tyr
            20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 144:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 36
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAG   36
Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
 1   5   10

154

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 145:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```
AAG CAT CTT GGG ATT GAA TTT ATG GAG                    27
Lys His Leu Gly Ile Glu Phe Met Glu
 1               5
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 146:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 569
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```
AAA GCG GAG GAG CTC TAC CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT    48
Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile
 1               5                  10                  15

TGC ATC GCG CTG CTC GTG GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC    96
Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Val Tyr Cys
                20                  25                  30

AAA ACC AAG AAA CAA CGG AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC   144
Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln Ser
                35                  40                  45

CTT CGG TCT GAA AGA AAC ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC   192
Leu Arg Ser Glu Arg Asn Thr Met Met Asn Val Ala Asn Gly Pro His
            50                  55                  60

CAC CCC AAT CCG CCC CCC GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA   240
His Pro Asn Pro Pro Pro Glu Asn Val Gln Leu Val Asn Gln Tyr Val
 65                  70                  75                  80

TCT AAA AAT GTC ATC TCT AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG   288
Ser Lys Asn Val Ile Ser Ser Glu His Ile Val Glu Arg Glu Ala Glu
                85                  90                  95

AGC TCT TTT TCC ACC AGT CAC TAC ACT TCG ACA GCT CAT CAT TCC ACT   336
S r Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Ala His His Ser Thr
            100                 105                 110
```

155

```
ACT GTC ACT CAG ACT CCC AGT CAC AGC TGG AGC AAT GGA CAC ACT GAA          384
Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly His Thr Glu
        115             120             125

AGC ATC ATT TCG GAA AGC CAC TCT GTC ATC GTG ATG TCA TCC GTA GAA          432
Ser Ile Ile Ser Glu Ser His Ser Val Ile Val Met Ser Ser Val Glu
        130             135             140

AAC AGT AGG CAC AGC AGC CCG ACT GGG GGC CCG AGA GGA CGT CTC AAT          480
Asn Ser Arg His Ser Ser Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn
145             150             155             160

GGC TTG GGA GGC CCT CGT GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA          528
Gly Leu Gly Gly Pro Arg Glu Cys Asn Ser Phe Leu Arg His Ala Arg
            165             170             175

GAA ACC CCT GAC TCC TAC CGA GAC TCT CCT CAT AGT G AAAG                   569
Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser
            180             185
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 147:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 730
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

```
G TAT GTA TCA GCA ATG ACC ACC CCG GCT CGT ATG TCA CCT GTA GAT          46
  Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp
  1               5               10              15

TTC CAC ACG CCA AGC TCC CCC AAG TCA CCC CCT TCG GAA ATG TCC CCG        94
Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro
            20              25              30

CCC GTG TCC AGC ACG ACG GTC TCC ATG CCC TCC ATG GCG GTC AGT CCC        142
Pro Val Ser Ser Thr Thr Val Ser Met Pro Ser Met Ala Val Ser Pro
            35              40              45

TTC GTG GAA GAG GAG AGA CCC CTG CTC CTT GTG ACG CCA CCA CGG CTG        190
Phe Val Glu Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu
        50              55              60

CGG GAG AAG TAT GAC CAC CAC GCC CAG CAA TTC AAC TCG TTC CAC TGC        238
Arg Glu Lys Tyr Asp His His Ala Gln Gln Phe Asn Ser Phe His Cys
        65              70              75
```

156

```
AAC CCC GCG CAT GAG AGC AAC AGC CTG CCC CCC AGC CCC TTG AGG ATA        286
Asn Pro Ala His Glu Ser Asn Ser Leu Pro Pro Ser Pro Leu Arg Ile
 80              85                  90                  95

GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG GAG TAC GAA CCA GCT CAA        334
Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln
                100                 105                 110

GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC CGG CGG GCC AAA AGA ACC        382
Glu Pro Val Lys Lys Leu Thr Asn Ser Ser Arg Arg Ala Lys Arg Thr
            115                 120                 125

AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG GAA ATG GAC AAC AAC ACA        430
Lys Pro Asn Gly His Ile Ala His Arg Leu Glu Met Asp Asn Asn Thr
            130                 135                 140

GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA ACA GAG GAT GAA AGA GTA        478
Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp Glu Arg Val
            145                 150                 155

GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG AAC CCC CTG GCA GCC AGT        526
Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln Asn Pro Leu Ala Ala Ser
160                 165                 170                 175

CTC GAG GCG GCC CCT GCC TTC CGC CTG GTC GAC AGC AGG ACT AAC CCA        574
Leu Glu Ala Ala Pro Ala Phe Arg Leu Val Asp Ser Arg Thr Asn Pro
                180                 185                 190

ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG CAG GCC AGG CTC TCC GGT        622
Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu Gln Ala Arg Leu Ser Gly
                195                 200                 205

GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC TAAAACCGAA ATACACCCAT         672
Val Ile Ala Asn Gln Asp Pro Ile Ala Val
            210                 215

AGATTCACCT GTAAAACTTT ATTTTATATA ATAAAGTATT CCACCTTAAA TTAAACAA        730
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 148:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1652
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:


```
AGTTTCCCCC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC        60
GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC       120
TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC       180
```

157

```
CCAGCGGCGC GCCAGCAGGA GCCACCCCGC GAGCGTGCGA CCGGGACGGA GCGCCCGCCA        240
GTCCCAGGTG GCCCGGACCG CACGTTGCGT CCCCGCGCTC CCCGCCGGCG ACAGGAGACG        300
CTCCCCCCCA CGCCGCGCGC GCCTCGGCCC GGTCGCTGGC CCGCCTCCAC TCCGGGGACA        360
AACTTTTCCC GAAGCCGATC CCAGCCCTCG ACCCAAACT TGTCGCGCGT CGCCTTCGCC        420
GGGAGCCGTC CGCGCAGAGC GTGCACTTCT CGGGCGAG ATG TCG GAG CGC AGA          473
                                          Met Ser Glu Arg Arg
                                           1                 5
```

```
GAA GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG        521
Glu Gly Lys Gly Lys Gly Lys Gly Gly Lys Lys Asp Arg Gly Ser Gly
                    10              15                  20
```

```
AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA GCC TTG CCT CCC        569
Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala Leu Pro Pro
                25              30              35
```

```
CGC TTG AAA GAG ATG AAG ATG CAG GAG TCT GTG GCA GGT TCC AAA CTA        617
Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Val Ala Gly Ser Lys Leu
            40              45              50
```

```
GTG CTT CGG TGC GAG ACC AGT TCT GAA TAC TCC TCT CTC AAG TTC AAG        665
Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys
        55              60              65
```

```
TGG TTC AAG AAT GGG AGT GAA TTA AGC CGA AAG AAC AAA CCA CAA AAC        713
Trp Phe Lys Asn Gly Ser Gly Leu Ser Arg Lys Asn Lys Pro Gln Asn
    70              75              80                  85
```

```
ATC AAG ATA CAG AAA AGG CCG GGG AAG TCA GAA CTT CGC ATT AGC AAA        761
Ile Lys Ile Gln Lys Arg Pro Gly Lys Ser Glu Leu Arg Ile Ser Lys
                90              95              100
```

```
GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA        809
Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys
            105             110             115
```

```
CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC        857
Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn
        120             125             130
```

```
GAG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT        905
Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser
    135             140             145
```

```
TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT        953
Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr
150             155             160             165
```

```
TCT TCA TCC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG       1001
Ser Ser Ser Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys
                170             175             180
```

158

```
TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC        1049
Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe
            185                 190                 195

ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG TGC AAG TGC CCA        1097
Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro
            200                 205                 210

AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC        1145
Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe
            215                 220                 225

TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAGGCGCATG            1193
Tyr S r Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
230                 235                 240

CTCAGTCGGT GCCGCTTTCT TGTTGCCGCA TCTCCCCTCA GATTCAACCT AGAGCTAGAT     1253
GCGTTTTACC AGGTCTAACA TTGACTGCCT CTGCCTGTCG CATGAGAACA TTAACACAAG     1313
CGATTGTATG ACTTCCTCTG TCCGTGACTA GTGGGCTCTG AGCTACTCGT AGGTGCGTAA     1373
GGCTCCAGTG TTTCTGAAAT TGATCTTGAA TTACTGTGAT ACGACATGAT AGTCCCTCTC     1433
ACCCAGTGCA ATGACAATAA AGGCCTTGAA AAGTCTCACT TTTATTGAGA AAATAAAAAT     1493
CGTTCCACGG GACAGTCCCT CTTCTTTATA AAATGACCCT ATCCTTGAAA AGGAGGTGTG     1553
TTAAGTTGTA ACCAGTACAC ACTTGAAATG ATGGTAAGTT CGCTTCGGTT CAGAATGTGT     1613
TCTTTCTGAC AAATAAACAG AATAAAAAAA AAAAAAAAA A                          1652
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 149:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1140
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```
CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG        48
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
1               5                   10                  15

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC        96
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
            20                  25                  30

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG       144
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
            35                  40                  45

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC       192
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro
            50                  55                  60
```

159

```
TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG        240
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val
65              70              75                  80

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG        288
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
            ·   85              90              95

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA        336
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
            100             105             110

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC        384
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser
            115             120             125

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG        432
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys
        130             135             140

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT        480
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr
145             150             155             160

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC        528
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
            165             170             175

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA        576
Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr
            180             185             190

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT        624
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
            195             200             205

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC        672
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
    210             215             220

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT        720
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
225             230             235             240

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT        768
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr
            245             250             255

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC        816
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser
            260             265             270


                              160
```

```
ACT CCC TTT CTG TCT CTG CCT GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG        870
Thr Pro Phe Leu Ser Leu Pro Glu
        275             280


TTGCCGCATC TCCCCTCAGA TTCCNCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT        930
GACTGCCTCT GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC        990
CGTGACTAGT GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG       1050
ATCTTGAATT ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG       1110
GCCTTGAAAA GTCAAAAAAA AAAAAAAAAA                                         1140




(2)   INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:      150:
      (i)  SEQUENCE CHARACTERISTICS:
           (A)  LENGTH:    1764
           (B)  TYPE: nucleic acid
           (C)  STRANDEDNESS:    single
           (D)  TOPOLOGY:   linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:


G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA          49
  Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu
  1                 5                 10                15

TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC            97
Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala
            20                25                30

AAC ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG          145
Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly
        35                40                45

ACA AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG          193
Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val
    50                55                60

AAT GGA GGC GAC TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA          241
Asn Gly Gly Asp Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg
65                70                75                80

TAC TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG          289
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu
                85                90                95

AAT GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC          337
Asn Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr
            100               105                110

CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT TGC ATC GCG CTG CTC GTG          385
Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val
        115               120               125
```

161

```
GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC AAA ACC AAG AAA CAA CGG       433
Val Gly Ile Met Cys Val Val Val Tyr Cys Lys Thr Lys Lys Gln Arg
    130             135             140

AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC CTT CGG TCT GAA AGA AAC       481
Lys Lys Leu His Asp Arg L u Arg Gln S r Leu Arg Ser Glu Arg Asn
145             150             155             160

ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC CAC CCC AAT CCG CCC CCC       529
Thr Met Met Asn Val Ala Asn Gly Pro His His Pro Asn Pro Pro Pro
                165             170             175

GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA TCT AAA AAT GTC ATC TCT       577
Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser
            180             185             190

AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG AGC TCT TTT TCC ACC AGT       625
Ser Glu His Ile Val Glu Arg Glu Ala Glu Ser Ser Phe Ser Thr Ser
            195             200             205

CAC TAC ACT TCG ACA GCT CAT CAT TCC ACT ACT GTC ACT CAG ACT CCC       673
His Tyr Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro
    210             215             220

AGT CAC AGC TGG AGC AAT GGA CAC ACT GAA AGC ATC ATT TCG GAA AGC       721
Ser His Ser Trp Ser Asn Gly His Thr Glu Ser Ile Ile Ser Glu Ser
225             230             235             240

CAC TCT GTC ATC GTG ATG TCA TCC GTA GAA AAC AGT AGG CAC AGC AGC       769
His Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser
                245             250             255

CCG ACT GGG GGC CCG AGA GGA CGT CTC AAT GGC TTG GGA GGC CCT CGT       817
Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Leu Gly Gly Pro Arg
                260             265             270

GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA GAA ACC CCT GAC TCC TAC       865
Glu Cys Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr
            275             280             285

CGA GAC TCT CCT CAT AGT GAA AGA CAT AAC CTT ATA GCT GAG CTA AGG       913
Arg Asp Ser Pro His Ser Glu Arg His Asn Leu Ile Ala Glu Leu Arg
    290             295             300

AGA AAC AAG GCC CAC AGA TCC AAA TGC ATG CAG ATC CAG CTT TCC GCA       961
Arg Asn Lys Ala His Arg Ser Lys Cys Met Gln Ile Gln Leu Ser Ala
305             310             315             320

ACT CAT CTT AGA GCT TCT TCC ATT CCC CAT TGG GCT TCA TTC TCT AAG      1009
Thr His Leu Arg Ala Ser Ser Ile Pro His Trp Ala Ser Phe Ser Lys
                325             330             335
```

162

```
ACC CCT TGG CCT TTA GGA AGG TAT GTA TCA GCA ATG ACC ACC CCG GCT         1057
Thr Pro Trp Pro Leu Gly Arg Tyr Val S r Ala Met Thr Thr Pro Ala
            340                 345             350

CGT ATG TCA CCT GTA GAT TTC CAC ACG CCA AGC TCC CCC AAG TCA CCC         1105
Arg Met Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro
            355                 360             365

CCT TCG GAA ATG TCC CCG CCC GTG TCC AGC ACG ACG GTC TCC ATG CCC.        1153
Pro Ser Glu Met Ser Pro Pro Val Ser Ser Thr Thr Val Ser Met Pro
            370                 375             380

TCC ATG GCG GTC AGT CCC TTC GTG GAA GAG GAG AGA CCC CTG CTC CTT         1201
Ser Met Ala Val Ser Pro Phe Val Glu Glu Glu Arg Pro Leu Leu Leu
385                 390                 395             400

GTG ACG CCA CCA CGG CTG CGG GAG AAG TAT GAC CAC CAC GCC CAG CAA         1249
Val Thr Pro Pro Arg Leu Arg Glu Lys Tyr Asp His His Ala Gln Gln
                405                 410             415

TTC AAC TCG TTC CAC TGC AAC CCC GCG CAT GAG AGC AAC AGC CTG CCC         1297
Phe Asn Ser Phe His Cys Asn Pro Ala His Glu Ser Asn Ser Leu Pro
                420                 425             430

CCC AGC CCC TTG AGG ATA GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG         1345
Pro Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln
                435                 440             445

GAG TAC GAA CCA GCT CAA GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC         1393
Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Thr Asn Ser Ser
450                 455                 460

CGG CGG GCC AAA AGA ACC AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG         1441
Arg Arg Ala Lys Arg Thr Lys Pro Asn Gly His Ile Ala His Arg Leu
465                 470                 475             480

GAA ATG GAC AAC AAC ACA GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA         1489
Glu Met Asp Asn Asn Thr Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu
                485                 490             495

ACA GAG GAT GAA AGA GTA GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG         1537
Thr Glu Asp Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln
            500                 505             510

AAC CCC CTG GCA GCC AGT CTC GAG GCG GCC CCT GCC TTC CGC CTG GTC         1585
Asn Pro Leu Ala Ala Ser Leu Glu Ala Ala Pro Ala Phe Arg Leu Val
            515                 520             525

GAC AGC AGG ACT AAC CCA ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG         1633
Asp Ser Arg Thr Asn Pro Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu
            530                 535             540
```

163

```
CAG GCC AGG CTC TCC GGT GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC          1681
Gln Ala Arg Leu Ser Gly Val Ile Ala Asn Gln Asp Pro Ile Ala Val
545                     550                 555                 560


TAAAACCGAA ATACACCCAT AGATTCACCT GTAAAACTTT ATTTTATATA ATAAAGTATT        1741
CCACCTTAAA TTAAACAAAA AAA                                                1764



(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:      151:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH:    50
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY:   linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:


Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
1               5               10              15


Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
            20              25              30


Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser
        35              40              45


Phe Tyr
    50



(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:      152:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH:    50
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY:   linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:


Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
1               5               10              15


Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
            20              25              30


Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro Met Lys
        35              40              45


Val Gln
    50
```

164

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 153:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

Glu Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His Gly Glu Cys Lys
1   5   10   15

Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys Lys Cys Gln Gln Glu Tyr
            20   25   30

Phe Gly Glu Arg Cys Gly Glu Lys Ser Asn Lys Thr His Ser
        35   40   45

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 154:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 198
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT   48
S r His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1   5   10   15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC   96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
                20   25   30

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC   144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
        35   40   45

GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT   192
Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro
    50   55   60

GAA TAG   198
Glu
65

165

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 155:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 192
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:


```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT          48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1               5                   10                  15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC          96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            20                  25                  30

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT         144
L u Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
        35                  40                  45

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC TAA         192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr
    50                  55                  60
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 156:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 183
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT          48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1               5                   10                  15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC          96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            20                  25                  30

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC         144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
        35                  40                  45

GTA ATG GCC AGC TTC TAC AAA GCG GAG GAG CTC TAC TAA                     183
Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr
    50                  55                  60
```

166

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 157:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 210
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:


```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT        48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1               5               10              15


GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC        96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            20              25              30


TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC       144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
        35              40              45


GTA ATG GCC AGC TTC TAC AAG CAT CTT GGG ATT GAA TTT ATG GAG AAA       192
Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Lys
    50              55              60


GCG GAG GAG CTC TAC TAA                                               210
Ala Glu Glu Leu Tyr
65
```


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 158:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 267
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:


```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT        48
S r His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1               5               10              15


GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC        96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            20              25              30


TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT       144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
        35              40              45
```

167

```
GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT        192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr
    50              55                  60

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC        240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Ph  Tyr Ser Thr Ser
65              70                  75                  80

ACT CCC TTT CTG TCT CTG CCT GAA TAG                                    267
Thr Pro Phe Leu Ser Leu Pro Glu
            85
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 159:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 252
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT        48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1               5                   10                  15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC        96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            20                  25                  30

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT        144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
        35                  40                  45

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT        192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr
    50              55                  60

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AAA GCG GAG        240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys Ala Glu
65              70                  75                  80

GAG CTC TAC TAA                                                        252
Glu Leu Tyr
```

168

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 160:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 128
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: singl
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:


```
CC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG TGT GCA         47
   Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys Cys Ala
   1               5               10              15

GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC ATG GTG         95
Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val
            20              25              30

AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG T GC                            128
Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
            35              40
```


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 161:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 141
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:


```
A CAT AAC CTT ATA GCT GAG CTA AGG AGA AAC AAG GCC CAC AGA TCC          46
  His Asn Leu Ile Ala Glu Leu Arg Arg Asn Lys Ala His Arg Ser
  1               5               10              15

AAA TGC ATG CAG ATC CAG CTT TCC GCA ACT CAT CTT AGA GCT TCT TCC        94
Lys Cys Met Gln Ile Gln Leu Ser Ala Thr His Leu Arg Ala Ser Ser
            20              25              30

ATT CCC CAT TGG GCT TCA TTC TCT AAG ACC CCT TGG CCT TTA GGA AG         141
Ile Pro His Trp Ala Ser Phe Ser Lys Thr Pro Trp Pro Leu Gly Arg
            35              40              45
```

169

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 162:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
   (ix) FEATURE:
        (D)   OTHER INFORMATION: Xaa in positions 15 and 22 is unknown.
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Ala Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Xaa Phe
 1   5   10   15

Met Val Lys Asp Leu Xaa Asn Pro
          20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 163:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 745
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

ATG AGA TGG CGA CGC GCC CCG CGC CGC TCC GGG CGT CCC GGC CCC CGG   48
Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg
 1   5   10   15

GCC CAG CGC CCC GGC TCC GCC GCC CGC TCG TCG CCG CCG CTG CCG CTG   96
Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu
         20   25   30

CTG CCA CTA CTG CTG CTG CTG GGG ACC GCG GCC CTG GCG CCG GGG GCG   144
Leu Pro Leu Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala
         35   40   45

GCG GCC GGC AAC GAG GCG GCT CCC GCG GGG GCC TCG GTG TGC TAC TCG   192
Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser
         50   55   60

TCC CCG CCC AGC GTG GGA TCG GTG CAG GAG CTA GCT CAG CGC GCC GCG   240
Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala
65   70   75   80

GTG GTG ATC GAG GGA AAG GTG CAC CCG CAG CGG CGG CAG CAG GGG GCA   288
Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala
               85   90   95

170

```
CTC GAC AGG AAG GCG GCG GCG GCG GCG GGC GAG GCA GGG GCG TGG GGC          336
Leu Asp Arg Lys Ala Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly
            100                     105                 110

GGC GAT CGC GAG CCG CCA GCC GCG GGC CCA CGG GCG CTG GGG CCG CCC          384
Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro
            115                     120                 125

GCC GAG GAG CCG CTG CTC GCC GCC AAC GGG ACC GTG CCC TCT TGG CCC          432
Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro
            130                     135                 140

ACC GCC CCG GTG CCC AGC GCC GGC GAG CCC GGG GAG GAG GCG CCC TAT          480
Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr
145                     150                 155                 160

CTG GTG AAG GTG CAC CAG GTG TGG GCG GTG AAA GCC GGG GGC TTG AAG          528
Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys
                165                 170                 175

AAG GAC TCG CTG CTC ACC GTG CGC CTG GGG ACC TGG GGC CAC CCC GCC          576
Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala
            180                     185                 190

TTC CCC TCC TGC GGG AGG CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC          624
Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe
            195                     200                 205

ATG GAG CCC GAC GCC AAC AGC ACC AGC CGC GCG CCG GCC GCC TTC CGA          672
Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Ala Phe Arg
210                     215                 220

GCC TCT TTC CCC CCT CTG GAG ACG GGC CGG AAC CTC AAG AAG GAG GTC          720
Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val
225                     230                 235                 240

AGC CGG GTG CTG TGC AAG CGG TGC G                                        745
Ser Arg Val Leu Cys Lys Arg Cys
                245
```

171

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 164:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: Xaa in position 1 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Xaa Ala Leu Ala Ala Ala Gly Tyr Asp Val Glu Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 165:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 5
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: Xaa in position 1 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Xaa Leu Val Leu Arg
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 166:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 11
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ix) FEATURE:
        (D) OTHER INFORMATION: Xaa in positions 1, 2, and 3 is unknown.
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Xaa Xaa Xaa Tyr Pro Gly Gln Ile Thr Ser Asn
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 167:
       (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 60
               (B) TYPE: nucl ic acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear
       (ix) FEATURE:
               (D) OTHER INFORMATION: N in positions 25 and 36 is unknown.

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

ATAGGGAAGG GCGGGGGAAG GGTCNCCCTC NGCAGGGCCG GGCTTGCCTC TGGAGCCTCT   60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 168:
       (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 18
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear
       (ix) FEATURE:
               (D) OTHER INFORMATION: N in position 16 is unknown.
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

TTTACACATA TATTCNCC 18

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 169:
       (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 21
               (B) TYPE: amino acid
               (C) STRANDEDNESS:
               (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

Glu Thr Gln Pro Asp Pro Gly Gln Ile Leu Lys Lys Val Pro Met Val
  1   5   10   15

Ile Gly Ala Tyr Thr
              20

173

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 170:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 422
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg
 1   5   10   15

Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu
             20   25   30

Leu Pro Leu Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala
         35   40   45

Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser
     50   55   60

Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala
 65   70   75   80

Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala
             85   90   95

Leu Asp Arg Lys Ala Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly
         100   105   110

Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro
         115   120   125

Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro
     130   135   140

Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr
 145   150   155   160

Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys
             165   170   175

Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala
         180   185   190

Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe
         195   200   205

Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Ala Phe Arg
     210   215   220

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```
Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val
225                 230                 235                 240

Ser Arg Val Leu Cys Lys Arg Cys Ala Leu Pro Pro Gln Leu Lys Glu
                245                 250                 255

Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu Val Leu Arg Cys
                260                 265                 270

Glu Thr Ser Ser Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn
                275                 280                 285

Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln
    290                 295                 300

Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn Lys Ala Ser Leu Ala
305                 310                 315                 320

Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp
                325                 330                 335

Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr
                340                 345                 350

Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys
                355                 360                 365

Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser
    370                 375                 380

Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp
385                 390                 395                 400

Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro
                405                 410                 415

Phe Leu Ser Leu Pro Glu
                420
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 171:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 69
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

```
Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
  1             5                 10                  15
```

175

```
Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
            20                25                30

Pro Arg Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr
            35                40                45

Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala
    50                55                60

Asn Thr Ser Ser Ser
65
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 172:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 19
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

```
Arg Lys Gly Asp Val Pro Gly Pro Arg Val Lys Ser Ser Arg Ser Thr
 1               5               10                  15

Thr Thr Ala
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 173:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 231
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

```
CGCGAGCGCC TCAGCGCGGC CGCTCGCTCT CCCCCTCGAG GGACAAACTT TTCCCAAACC      60
CGATCCGAGC CCTTGGACCA AACTCGCCTG CGCCGAGAGC CGTCCGCGTA GAGCGCTCCG     120
TCTCCGGCGA GATGTCCGAG CGCAAAGAAG GCAGAGGCAA AGGGAAGGGC AAGAAGAAGG     180
AGCGAGGCTC CGGCAAGAAG CCGGAGTCCG CGGCGGGCAG CCAGAGCCCA G             231
```

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 174:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 178
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

CCTTGCCTCC CCGATTGAAA GAGATGAAAA GCCAGGAATC GGCTGCAGGT TCCAAACTAG   60
TCCTTCGGTG TGAAACCAGT TCTGAATACT CCTCTCTCAG ATTCAAGTGG TTCAAGAATG   120
GGAATGAATT GAATCGAAAA AACAAACCAC AAAATATCAA GATACAAAAA AAGCCAGG   178

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 175:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 122
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

GAAGTCAGAA CTTCGCATTA ACAAAGCATC ACTGGCTGAT TCTGGAGAGT ATATGTGCAA   60
AGTGATCAGC AAATTAGGAA ATGACAGTGC CTCTGCCAAT ATCACCATCG TGGAATCAAA   120
CG   122

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 176:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 102
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

AGATCATCAC TGGTATGCCA GCCTCAACTG AAGGAGCATA TGTGTCTTCA GAGTCTCCCA   60
TTAGAATATC AGTATCCACA GAAGGAGCAA ATACTTCTTC AT   102

177

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 177:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 128
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

CTACATCTAC ATCCACCACT GGGACAAGCC ATCTTGTAAA ATGTGCGGAG AAGGAGAAAA   60
CTTTCTGTGT GAATGGAGGG GAGTGCTTCA TGGTGAAAGA CCTTTCAAAC CCCTCGAGAT   120
ACTTGTGC   128

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 178:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 69
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

AAGTGCCAAC CTGGATTCAC TGGAGCAAGA TGTACTGAGA ATGTGCCCAT GAAAGTCCAA   60
AACCAAGAA   69

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 179:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

TCGGGCTCCA TGAAGAAGAT GTA   23

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 180
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

TCCATGAAGA AGATGTACCT GCT   23

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 181
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ATGTACCTGC TGTCCTCCTT GA   22

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 182
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

TTGAAGAAGG ACTCGCTGCT CA   22

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 183
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

AAAGCCGGGG GCTTGAAGAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 184
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

ATGARGTGTG GGCGGCGAAA   20